

FIG. 1

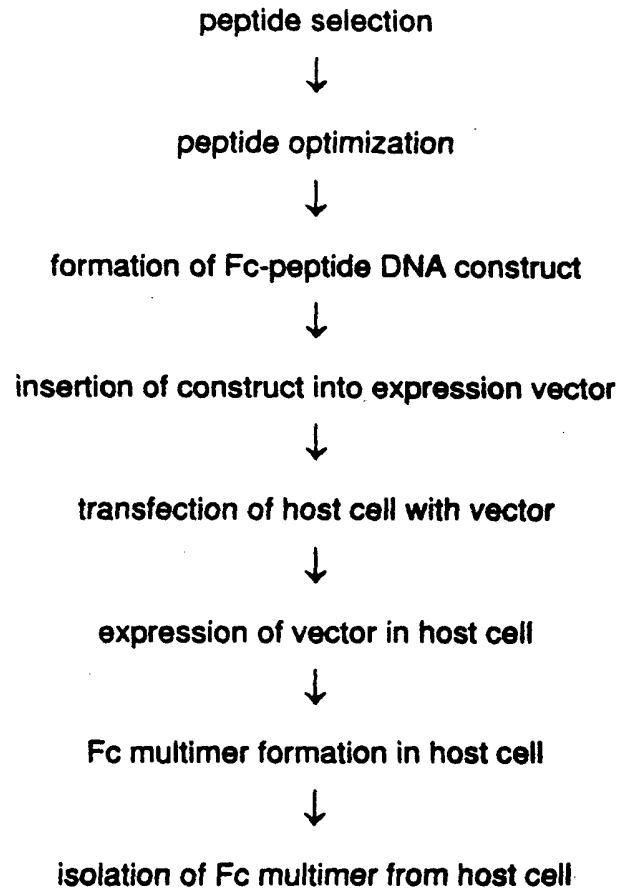


FIG. 2A

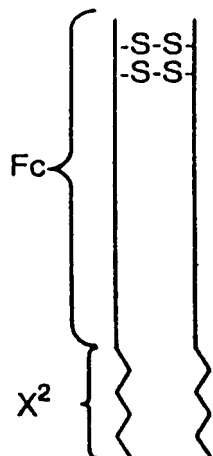


FIG. 2B

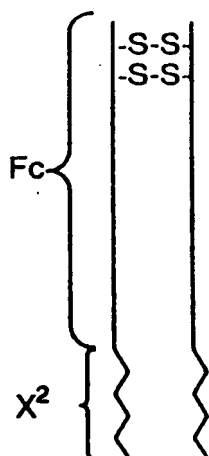


FIG. 2C

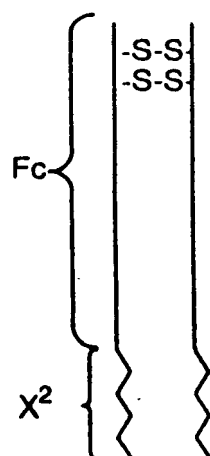


FIG. 2D

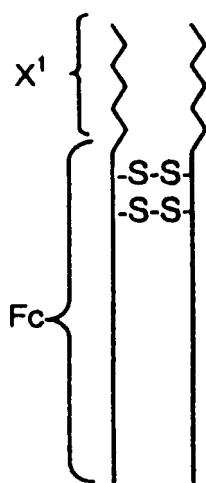


FIG. 2E

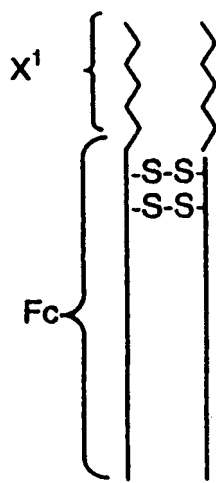


FIG. 2F

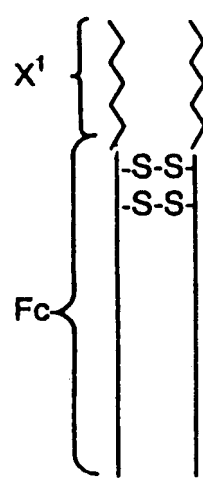


FIG. 3A



FIG. 3B

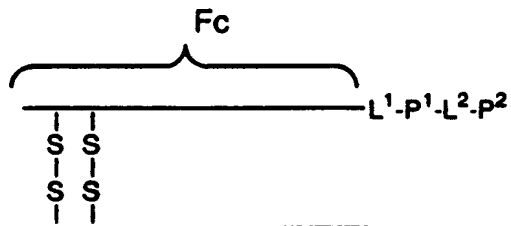


FIG. 3C

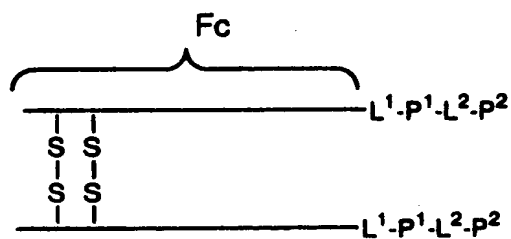


FIG. 4

```

1  ATGGACAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCGTCA
   +-----+-----+-----+-----+-----+-----+-----+
a  M D K T H T C P P C P A P E L L G G P S
   +-----+-----+-----+-----+-----+-----+-----+
61  GTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
   +-----+-----+-----+-----+-----+-----+-----+
a  CAGAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG
   +-----+-----+-----+-----+-----+-----+-----+
121  ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
   +-----+-----+-----+-----+-----+-----+-----+
a  TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC
   +-----+-----+-----+-----+-----+-----+-----+
181  T C V V V D V S H E D P E V K F N W Y V
   +-----+-----+-----+-----+-----+-----+-----+
a  GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
   +-----+-----+-----+-----+-----+-----+-----+
241  CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC
   +-----+-----+-----+-----+-----+-----+-----+
a  D G V E V H N A K T K P R E E Q Y N S T
   +-----+-----+-----+-----+-----+-----+-----+
241  TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
   +-----+-----+-----+-----+-----+-----+-----+
a  ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCTCTCATG
   +-----+-----+-----+-----+-----+-----+-----+
301  Y R V V S V L T V L H Q D W L N G K E Y
   +-----+-----+-----+-----+-----+-----+-----+
a  AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCC
   +-----+-----+-----+-----+-----+-----+-----+
361  TTCACGTTCCAGAGGTTGTTTCGGGAGGGTTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG
   +-----+-----+-----+-----+-----+-----+-----+
a  K C K V S N K A L P A P I E K T I S K A
   +-----+-----+-----+-----+-----+-----+-----+
361  AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
   +-----+-----+-----+-----+-----+-----+-----+
a  TTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG
   +-----+-----+-----+-----+-----+-----+-----+
421  K G Q P R E P Q V Y T L P P S R D E L T
   +-----+-----+-----+-----+-----+-----+-----+
a  AAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
   +-----+-----+-----+-----+-----+-----+-----+
481  TTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC
   +-----+-----+-----+-----+-----+-----+-----+
a  K N Q V S L T C L V K G F Y P S D I A V
   +-----+-----+-----+-----+-----+-----+-----+
481  GAGTGGGAGAGCAATGGGCAGCCGGAACAACATAAGACCACGCCCTCCCGTGCTGGAC
   +-----+-----+-----+-----+-----+-----+-----+
a  CTCACCCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGACCTG
   +-----+-----+-----+-----+-----+-----+-----+
541  E W E S N G Q P E N N Y K T T P P V L D
   +-----+-----+-----+-----+-----+-----+-----+
a  TCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
   +-----+-----+-----+-----+-----+-----+-----+
601  AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC
   +-----+-----+-----+-----+-----+-----+-----+
a  S D G S F F L Y S K L T V D K S R W Q Q
   +-----+-----+-----+-----+-----+-----+-----+
601  GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
   +-----+-----+-----+-----+-----+-----+-----+
a  CCCTTGCAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTC
   +-----+-----+-----+-----+-----+-----+-----+
661  G N V F S C S V M H E A L H N H Y T Q K
   +-----+-----+-----+-----+-----+-----+-----+
684  AGCCTCTCCCTGTCTCCGGGTAAA
   +-----+-----+-----+-----+-----+-----+-----+
TCCGAGAGGGACAGAGGCCCATTT

```

FIG. 5

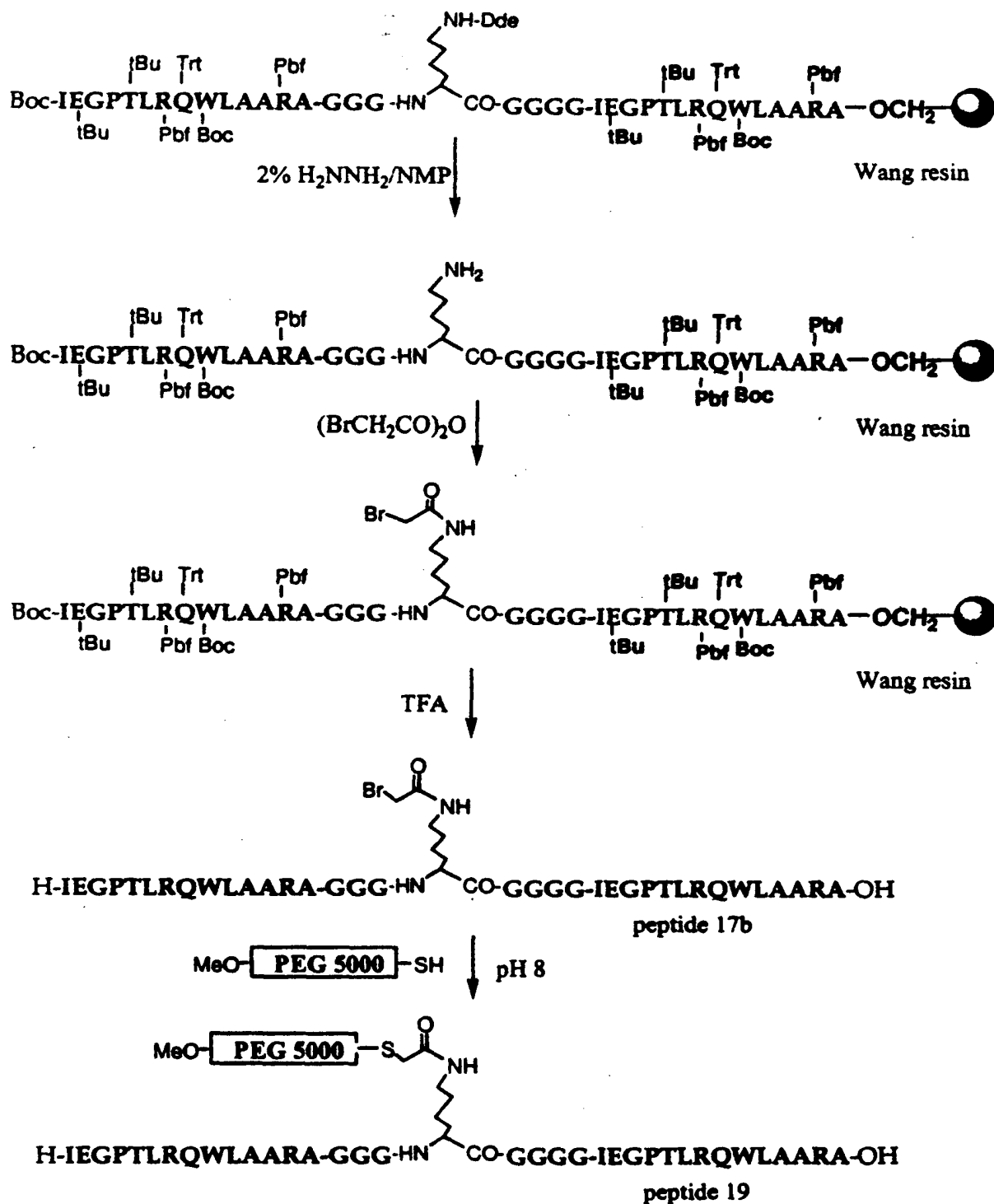


FIG. 6

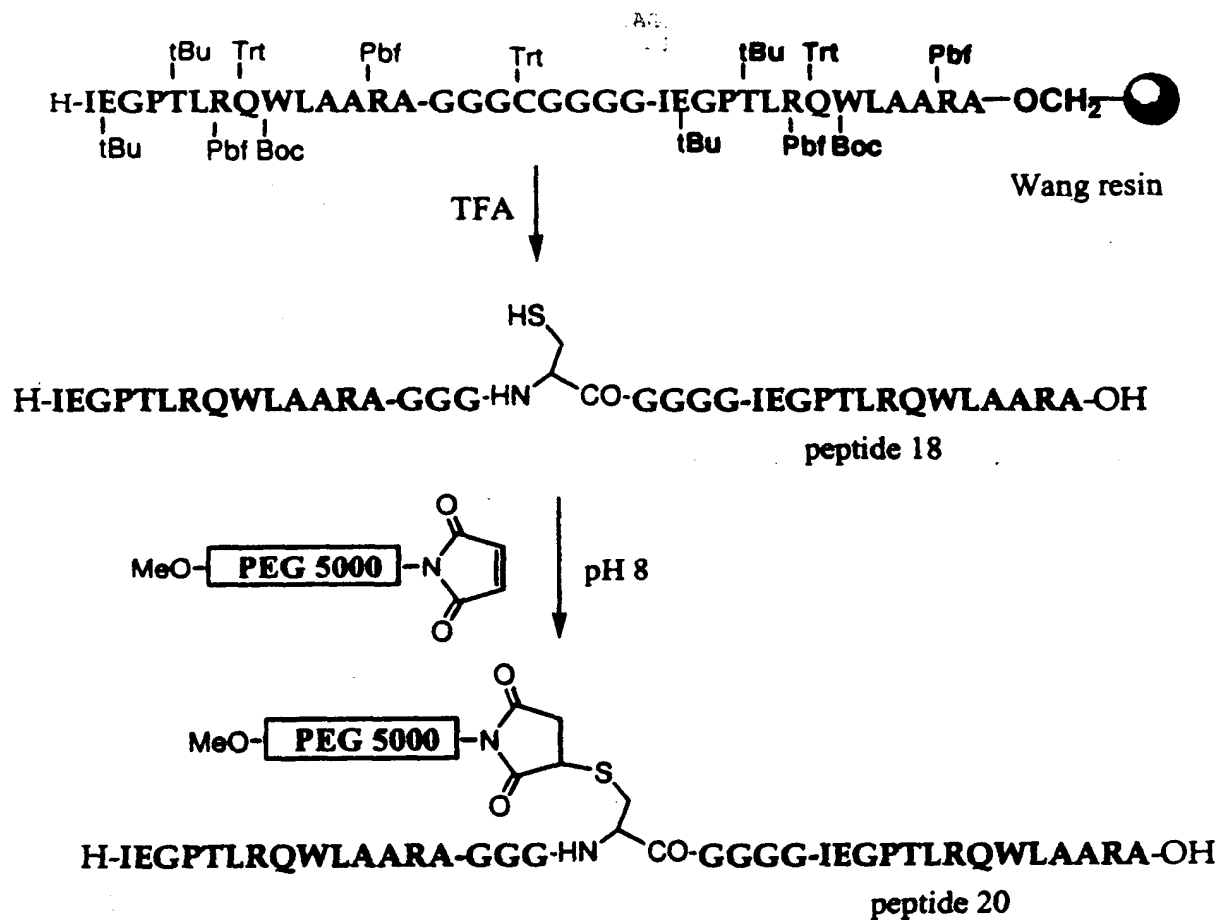


FIG. 7

XbaI
|
1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC 60
AGATCTAAACAAAATTGATTAATTTCTCTTATTGTATACCTGTTTTGAGTGTGTACAG
M D K T H T C P -

61 CACCTTGTCAGCTCCGGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAC 120
GTGGAACAGGTCGAGGCCTTGAGGACCCCTGGGAGTCAGAAGGAGAAGGGGGTTTTG
P C P A P E L L G G P S V F L F P P K P -

121 CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA 180
GGTTCTGTGGGAGTACTAGAGGCCTGGGAGTCCAGTGTACGCACCACCACCTGCACT
K D T L M I S R T P E V T C V V V D V S -

181 GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
H E D P E V K F N W Y V D G V E V H N A -

241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTCA 300
GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGTCATGGCACACCAGTCGCAGGAGT
K T K P R E E Q Y N S T Y R V V S V L T -

301 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG 360
GGCAGGACGTGGTCCTGACCGACTTACCGTTCTCATGTTTACGTTCCAGAGGTGTTTC
V L H Q D W L N G K E Y K C K V S N K A -

361 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC 420
GGGAGGGTCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
L P A P I E K T I S K A K G Q P R E P Q -

421 AGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTACGCCTGACCT 480
TCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
V Y T L P P S R D E L T K N Q V S L T C -

481 GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG
L V K G F Y P S D I A V E W E S N G Q P -

541 CGGAGAACAACACTACAAGACCACGCCTCCCGTGGTGGACTCCGACGGCTCCTTCTCTCT 600
GCCTCTTGTGATGTTCTGGTGGGAGGGCAGGACCTGAGGCTGCCGAGGAAGAAGGAGA
E N N Y K T T P P V L D S D G S F F L Y -

601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG 660
TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTTCCCTTGCAGAAGAGTACGAGGC
S K L T V D K S R W Q Q G N V F S C S V -

661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA 720
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
M H E A L H N H Y T Q K S L S L S P G K -

721 AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCTT 780
TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGAGTCACCGACCGACGAGCAGCAA
G G G G G I E G P T L R Q W L A A R A * -

BamHI
|
781 AATCTCGAGGATCC 794
TTAGAGCTCCTAGG

A ☆ -

FIG. 10

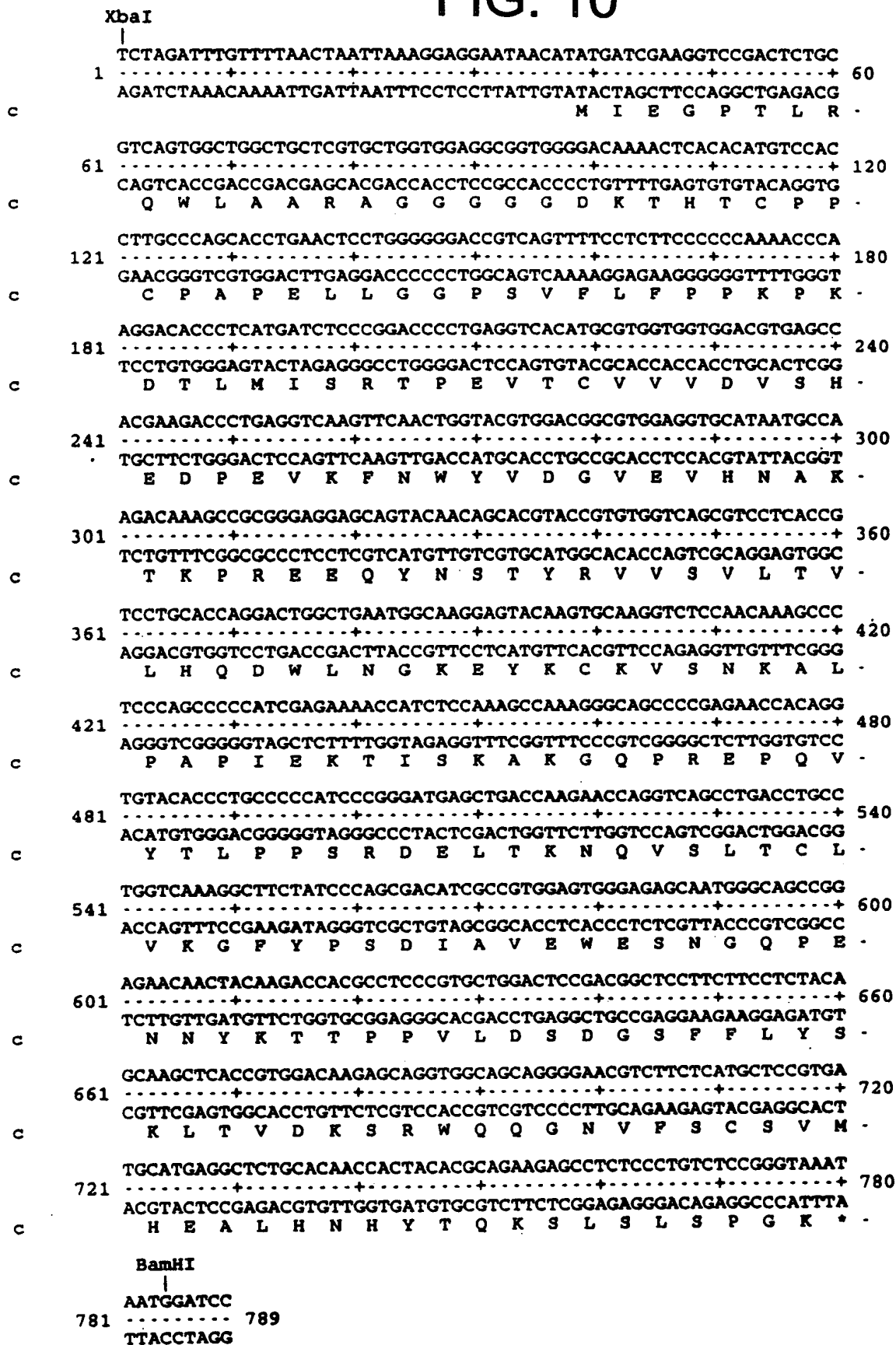


FIG.11

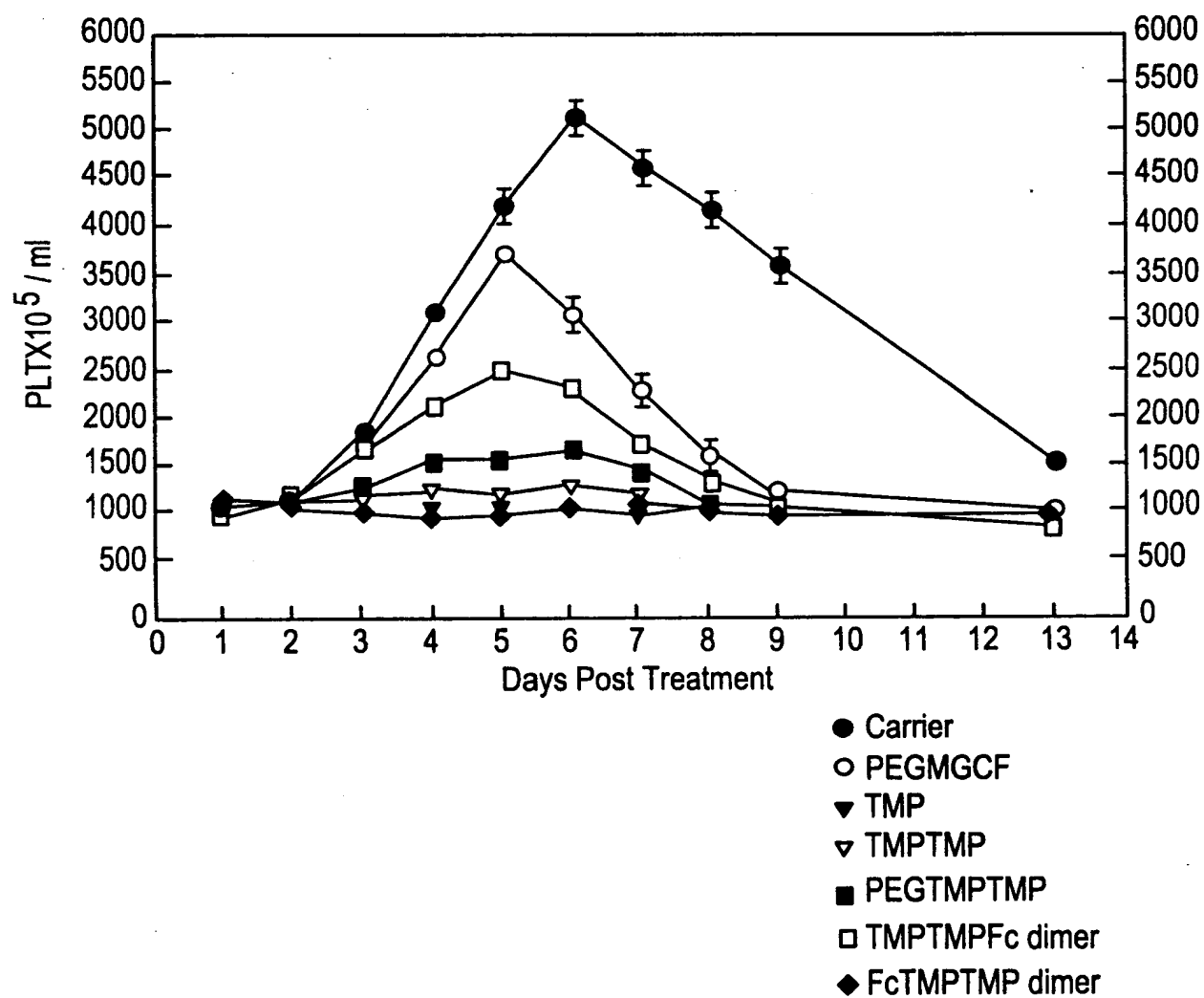


FIG.12

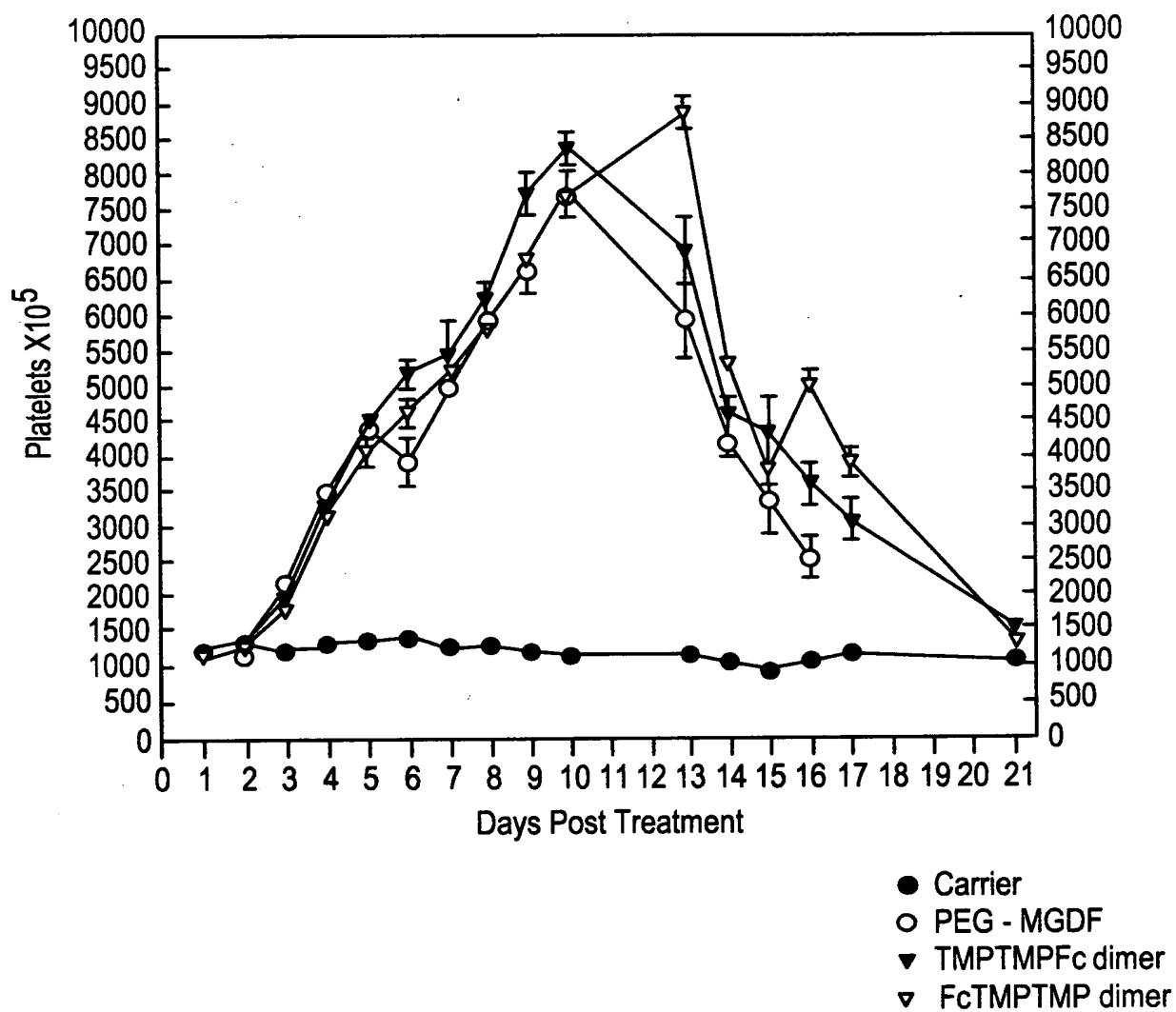


FIG. 13

XbaI
|

1 TCTAGATTTGTTTTAACTAATTAAGGAGGAATAACATATGGACAAAACCTCACACATGTC 60
AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTGTTTTGAGTGTGTACAG
CACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAC
61 GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTG 120
P C P A P E L L G G P S V F L F P P K P
CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
121 GGTTCCTGTGGGAGTACTAGAGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT 180
K D T L M I S R T P E V T C V V V D V S
GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
181 CCGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC 240
H E D P E V K F N W Y V D G V E V H N A
CCAAGACAAAGCCCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTCA
241 GGTTCGTGTTTCGGCGCCCTCTCGTCATGTTGTGTCGTCATGGCACACCAGTCCGAGGAGT 300
K T K P R E E Q Y N S T Y R V V S V L T
CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAG
301 GGCAGGACGTGGTCTCTGACCGACTTACCGTTCTCTCATGTTACGTTCCAGAGGTTGTTTC 360
V L H Q D W L N G K E Y K C K V S N K A
CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
361 GGGAGGGTTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCCGGGCTCTTGGTG 420
L P A P I E K T I S K A K G Q P R E P Q
AGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCTAGCCTGACCT
421 TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCCGACTGGA 480
V Y T L P P S R D E L T K N Q V S L T C
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCGAC
481 CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG 540
L V K G F Y P S D I A V E W E S N G Q P
CGGAGAACAACCTACAAGACCACGCCTCCCGTGTGACTCCGACGGCTCCTTCTTCTCTCT
541 GCCTCTTGTGATGTTCTTGGTGGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA 600
E N N Y K T T P P V L D S D G S F F L Y
ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
601 TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC 660
S K L T V D K S R W Q Q G N V F S C S V
TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
661 ACTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT 720
M H E A L H N H Y T Q K S L S L S P G K
AAGGTGGAGGTGGTGGTGGAGGTACTTACTCTTGCCACTTCGGCCCGCTGACTTGGGTTT
721 TTCCACCTCCACCACCACCTCCATGAATGAGAACGGTGAAGCCGGGCGACTGAACCCAAA 780
G G G G G G G T Y S C H F G P L T W V C
BamHI
|

781 GCAAACCGCAGGGTGGTTAATCTCGTGATCC 812
CGTTTGGCGTCCCACCAATTAGAGCACCTAGG
K P Q G G *

FIG. 14

XbaI
|

1 TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGGAGGTACTTACTCTTGCC 60
AGATCTAAACAAAATTGATTAATTTCTCTTATTGTATACCCTCCATGAATGAGAACGG
M G G T Y S C H -

61 ACTTCGGCCCCGCTGACTTGGGTATGTAAGCCACAAGGGGGTGGGGAGGCGGGGGGACA 120
TGAAGCCGGGCGACTGAACCCATACATTGGGTGTTCCCCACCCCCTCCGCCCCCCTGT
F G P L T W V C K P Q G G G G G G D K -

121 AAACCTCACACATGTCCACCTTGCCAGCACCTGAACCTCTGGGGGACCGTCAGTTTTC 180
TTTGAGTGTGTACAGGTGGAACGGGTGCTGGACTTGAGGACCCCCTGGCAGTCAAAGG
T H T C P P C P A P E L L G G P S V F L -

181 TCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCG 240
AGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGACTCCAGTGTACGC
P P P K P K D T L M I S R T P E V T C V -

241 TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 300
ACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGC
V V D V S H E D P E V K F N W Y V D G V -

301 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG 360
ACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCAC
E V H N A K T K P R E E Q Y N S T Y R V -

361 TGGTCAGCGTCTCACCCTGTCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA 420
ACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTCATGTTACGT
V S V L T V L H Q D W L N G K E Y K C K -

421 AGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGC 480
TCCAGAGGTTGTTTCGGGAGGGTCCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCG
V S N K A L P A P I E K T I S K A K G Q -

481 AGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACC 540
TCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTCTTGG
P R E P Q V Y T L P P S R D E L T K N Q -

541 AGGTCAGCCTGACCTGCCCTGGTCAAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGG 600
TCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCC
V S L T C L V K G P Y P S D I A V E W E -

601 AGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG 660
TCTCGTTACCCGTCCGCCTCTTGTGATGTTCTGGTGGGAGGGCAGACCTGAGGCTGC
S N G Q P E N N Y K T T P P V L D S D G -

661 GCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG 720
CGAGGAAGAAGGAGATGTCGTTTCAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGC
S F F L Y S K L T V D K S R W Q Q G N V -

721 TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT 780
AGAAGAGTACGAGGCACTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGA
F S C S V M H E A L H N H Y T Q K S L S -

BamHI
|

781 CCCTGTCTCCGGGTAAATAATGGATCC 807
GGGACAGAGGCCCATTTATTACCTAGG
L S P G K *

FIG. 15

XbaI
|
1 TCTAGATTTGAGTTTAACTTTTAGAAGGAGGAATAAAATATGGGAGGTACTTACTCTTG 60
AGATCTAAACTCAAAATGAAAATCTTCCTCCTTATTTTATACCTCCATGAATGAGAAC
M G G T Y S C -
b
61 CCACTTCGGCCCACTGACTTGGGTTTGCAAACCGCAGGGTGGCGGCGGCGGCGGCGGTGG 120
GGTGAAGCCGGGTGACTGAACCCAAACGTTTGGCGTCCCACCGCCGCGCGCGCCGCCACC
H F G P L T W V C K P Q G G G G G G G G -
b
121 TACCTATTCTGTCAATTTTGGCCCGCTGACCTGGGTATGTAAGCCACAAGGGGGTGGGG 180
ATGGATAAGGACAGTAAAACCGGGCGACTGGACCCATACATTCCGTGTTCCCCACCCCC
T Y S C H F G P L T W V C K P Q G G G G -
b
181 AGGCGGGGGGACAAAACCTCACACATGTCCACCTTGCCAGCACCTGAACTCCTGGGGGG 240
TCCGCCCCCCTGTTTGTAGTGTGTACAGGTGGAACGGGTCTGGACTTGAGGACCCCC
G G G D K T H T C P P C P A P E L L G G -
b
241 ACCGTCAGTTTCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCC 300
TGGCAGTCAAAAGGAGAAGGGGGGTTTGGGTCTCTGTGGGAGTACTAGAGGGCCTGGGG
P S V F L F P P K P K D T L M I S R T P -
b
301 TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG 360
ACTCCAGTGACGCACCCACCTGCACCTCGGTGCTTCTGGGACTCCAGTTCAAGTTGAC
E V T C V V V D V S H E D P E V K F N W -
b
361 GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAA 420
CATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCCGGCGCCTCCTCGTCAATGT
Y V D G V E V H N A K T K P R E E Q Y N -
b
421 CAGCACGTACCGTGTGGTCAGCGTCTCACCCTGCTGCACCAGGACTGGCTGAATGGCAA 480
GTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTT
S T Y R V V S V L T V L H Q D W L N G K -
b
481 GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTC 540
CCTCATGTTACGTTCCAGAGGTTGTTTCCGGAGGGTCCGGGGTAGCTCTTTTGGTAGAG
E Y K C K V S N K A L P A P I E K T I S -
b
541 CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGATGA 600
GTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACT
K A K G Q P R E P Q V Y T L P P S R D E -
b
601 GCTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACAT 660
CGACTGGTCTTGGTCCAGTCGACTGGACGGACAGTTTCCGAAGATAGGGTCCGCTGTA
L T K N Q V S L T C L V K G F Y P S D I -
b
661 CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATAAGACCACGCCTCCCGT 720
GCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTGTTGATGTTCTGGTGGGAGGGCA
A V E W E S N G Q P E N N Y K T T P P V -
b
721 GCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG 780
CGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCAC
L D S D G S F F L Y S K L T V D K S R W -
b
781 GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC 840
CGTCGTCCTTGCAGAAGAGTACGAGGCACTACTCCGAGACGTGTTGGTGATGTG
Q Q G N V F S C S V M H E A L H N H Y T -
b
BamHI
|
841 GCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC 881
CGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
Q K S L S L S P G K *

FIG. 16

XbaI
|

1 TCTAGATTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACACACATGTC 60
AGATCTAAACAAAATTGATTAATTTCTCTTATTGTATACCTGTTTGGAGTGTGTACAG
M D K T H T C P -

61 CACCTTGCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTCTCTTCCCCCAAAAC 120
GTGGAACGGGTCGTGGACTTGAGGACCCCTGGCAGTCAAAAGGAGAAGGGGGTTTTG
P C P A P E L L G G P S V F L F P P K P -

121 CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA 180
GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
K D T L M I S R T P E V T C V V V D V S -

181 GCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
H E D P E V K F N W Y V D G V E V H N A -

241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCA 300
GGTTCGTGTTTCGGCGCCCTCCTCGTCATGTTGTGTCGTGCATGGCACACCAGTCCGAGGAGT
K T K P R E E Q Y N S T Y R V V S V L T -

301 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAG 360
GGCAGGACGTGGTCTGACCGACTTACCGTTCCTCATGTTACGTTCCAGAGGTGTTTC
V L H Q D W L N G K E Y K C K V S N K A -

361 CCCTCCCAGCCCCATCGAGAAAACATCTCAAAGCCAAAGGGCAGCCCCGAGAACCAC 420
GGGAGGGTCGGGGTAGCTCTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
L P A P I E K T I S K A K G Q P R E P Q -

421 AGGTGTACACCCTGCCTCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT 480
TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCCGACTGGA
V Y T L P P S R D E L T K N Q V S L T C -

481 GCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTG
L V K G P Y P S D I A V E W E S N G Q P -

541 CGGAGAACAACACTACAAGACACGCCTCCCGTGTGACTCCGACGGCTCCTTCTTCTCT 600
GCCTCTTGTGATGTTCTGGTCCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
E N N Y K T T P P V L D S D G S F F L Y -

601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTTCTCATGTCCG 660
TGTCTGTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC
S K L T V D K S R W Q Q G N V F S C S V -

661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTA 720
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCAT
M H E A L H N H Y T Q K S L S L S P G K -

721 AAGGTGGAGGTGGTGGCGGAGGTACTTACTCTTGCCACTTCGGCCCACTGACTTGGGTTT 780
TTCCACCTCCACCACCGCTCATGAATGAGAACGGTGAAGCCGGGTGACTGAACCCAAA
G G G G G G G T Y S C H F G P L T W V C -

781 GCAAACCGCAGGTGGCGGGCGGGCGGGCGGTACCTATTCTGTCAATTTGGCCCGC 840
CGTTTGGCGTCCACCGCCGCGCGCGCCGCCACCATGGATAAGGACAGTAAACCGGGCG
K P Q G G G G G G G G T Y S C H F G P L -

BamHI
|

841 TGACCTGGGTATGTAAGCCACAAGGGGTTAATCTCGAGGATCC 884
ACTGGACCCATACATTGGTGTTCCTCCCAATTAGAGCTCCTAGG
T W V C K P Q G G *

FIG. 17A

[AatII sticky end] 5' GCGTAACGTATGCATGGTCTCC-
(position #4358 in pAMG21) 3' TGCACGCATTGCATACGTACCAGAGG-

-CCATGCGAGAGTAGGGAAGTCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-
-GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTCCGAGTCAGCTTTCTGA-
-GGGCCTTTCGTTTTATCTGTTGTTTGTGCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC-
-CCCGGAAAGCAAATAGACAACAAACAGCCACTTGCAGAGGACTCATCTGTTTAGGCG-
-CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCCG-
-GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCTCCACCGCCCGTCTGCGGGCG-
-CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTTGCGT-
-GTATTTGACGGTCCGTAGTTTAATTCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA-

AatII

-TTCTACAACTCTTTTGTTTATTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC-
-AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG-
-TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAAATTGCTTTAGAAATACTTTGGCAGC-
-AAAATTTTCATACCCGTTAGTTAACGAGGACAATTTAACGAAATCTTTATGAAACCGTCG-
-GGTTTGTTGTATTGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCGCTTAC-
-CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCACTGGCAGCGGAATG-
-TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCTTCGCATGCCCACGCTAAAC-
-ATGTCGGATTATAAAAACCTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTG-
-ATTCTTTTTCTCTTTTGTTAAATCGTTGTTTGATTTATTATTGCTATATTTATTTTTC-
-TAAGAAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAAACGATATAAATAAAAAG-
-GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTCATACACGCATGTAAAAATA-
-CTATTAATAGTTGATCTCTTCCTTGTTAATTACCATACAAGTATGTGCGTACATTTTTAT-
-AACTATCTATATAGTTGTCTTCTCTGAATGTGCAAACTAAGCATTCCGAAGCCATTAT-
-TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTTCGTAAGGCTTCGGTAATA-
-TAGCAGTATGAATAGGGAACTAAACCCAGTGATAAGACCTGATGATTTTCGCTTCTTTAA-
-ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAATT-
-TTACATTTGGAGATTTTTTATTTACAGCATTGTTTTCAAATATATTCCAATTAATCGGTG-
-AATGTAAACCTCTAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTAAATTAGCCAC-
-AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT-
-TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA-
-AATATTGCCTCCATTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG-
-TTATAACGGAGGTAAAAATCCCATTAATAGGTCTTAACCTTATAGTCTAAATTGGTATC-
-AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG-
-TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTTACATGGTAAATCAGTATAGTC-
-ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATTCTGT-
-TATTCGTAACCTAATTATAGTAATAACGAAGATGTCCGAAATTAATAAATTAATAAGACA-
-AAGTGTCGTCGGCATTATATGCTTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTC-
-TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG-
-GCAAGTTTTGCGTGTTATATATCATTAAAACGGTAATAGATTGACATTTGATTCTAATAA-
-CGTTCAAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAAACTAAGATTATT-

FIG. 17B

- ATTGGATTTTGTGACACTATTATATCGCTTGAAATACAATTGTTTAACATAAGTACCTG -
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC -

- TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTTGATT -
- ATCCTAGCATGTCCAAATGCGTTCCTTTACCAAACAATATCAGCTAATTAGCTAAACTAA -

- CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA -
- GATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT -

- GCTCACTAGTGTGCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA -
- CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT -

- GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA -
- CTTCTTCTTCTTCTTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT -

- ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTTGCTGAAAGGAGG -
- TGATCGTATTGGGGAACCCCGGAGATTGCCCAGAACTCCCCAAAAACGACTTTCCTCC -

- AACCGCTCTTCACGCTCTTCACGC 3' [SacII sticky end]
- TTGGCGAGAAGTGCGAGAAGTG 5' (position #5904 in pAMG21)

FIG.18A - 1

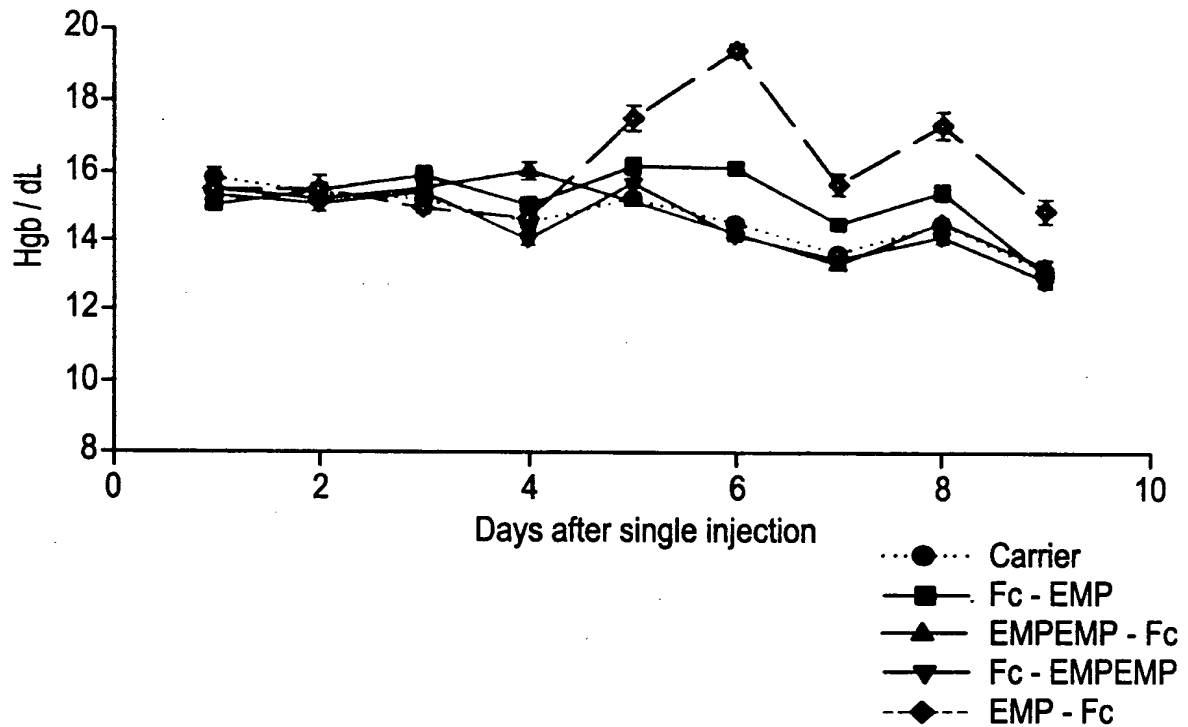


FIG.18A - 2

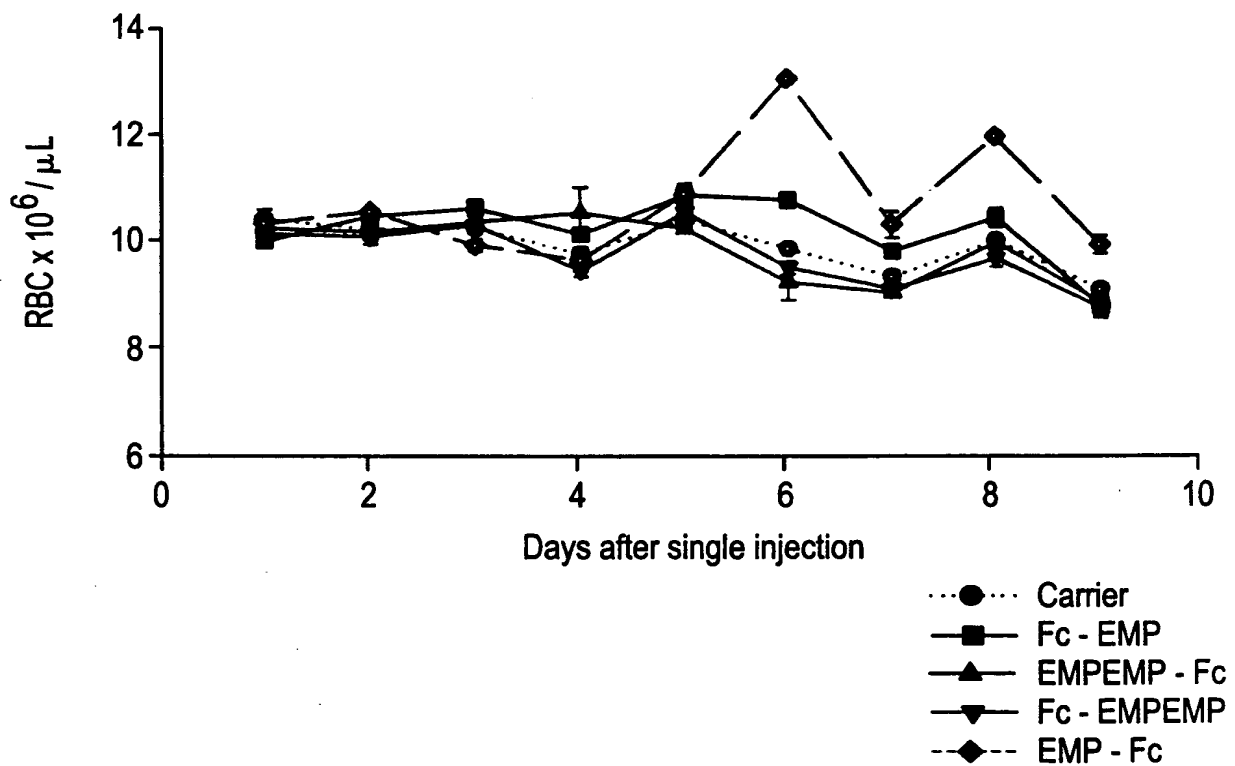


FIG.18A - 3

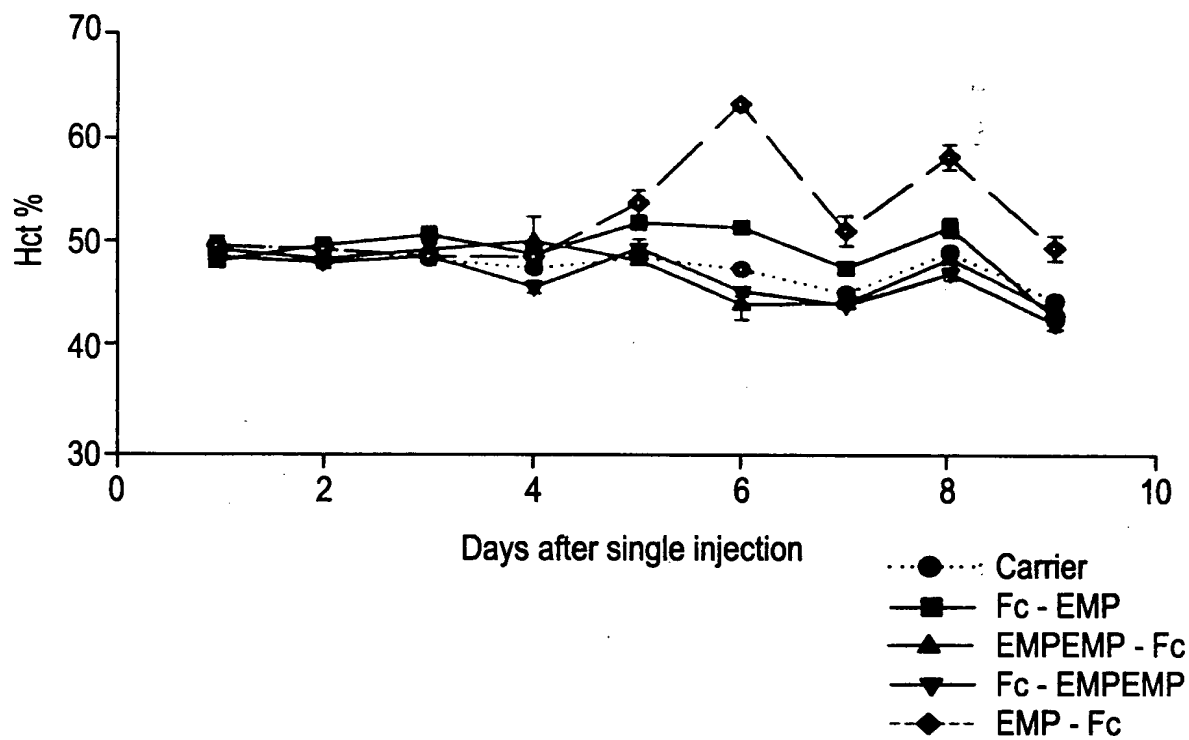


FIG.18B - 1

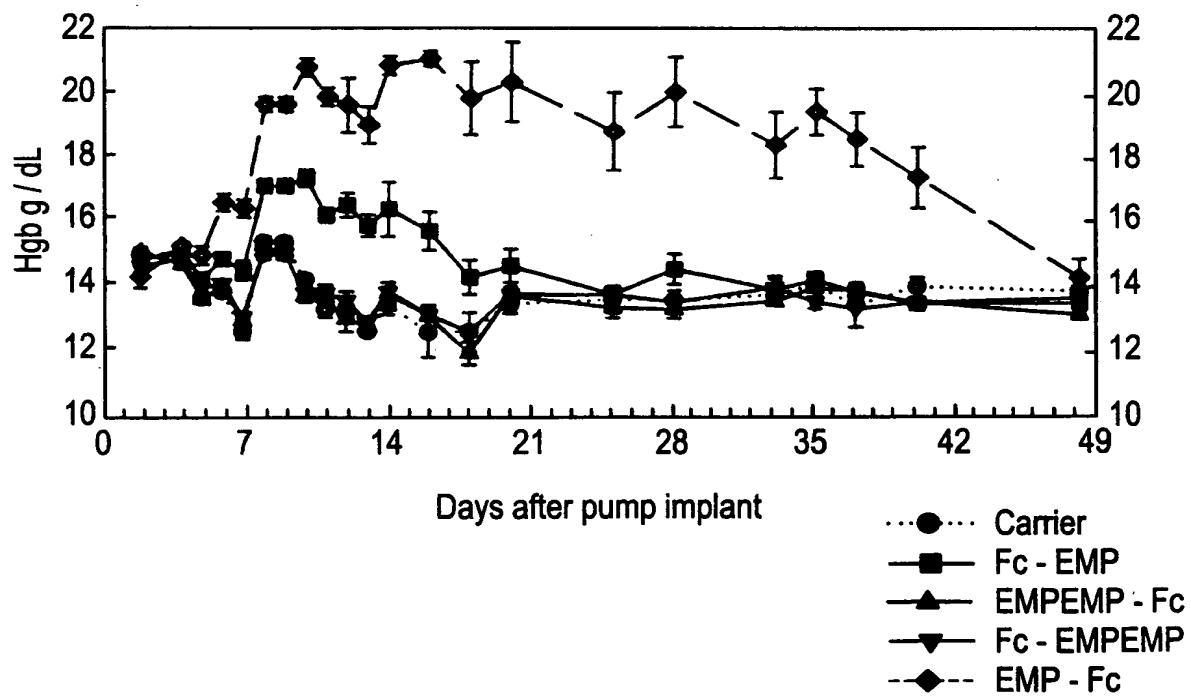


FIG.18B - 2

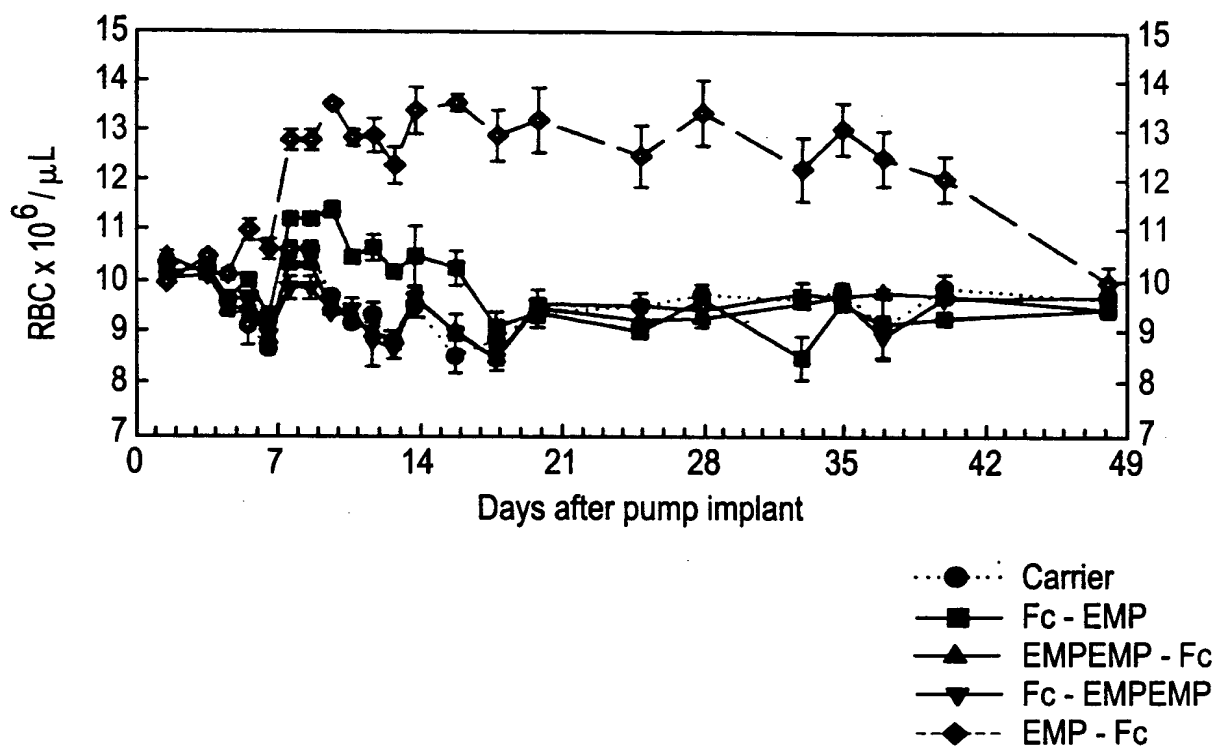


FIG.18B - 3

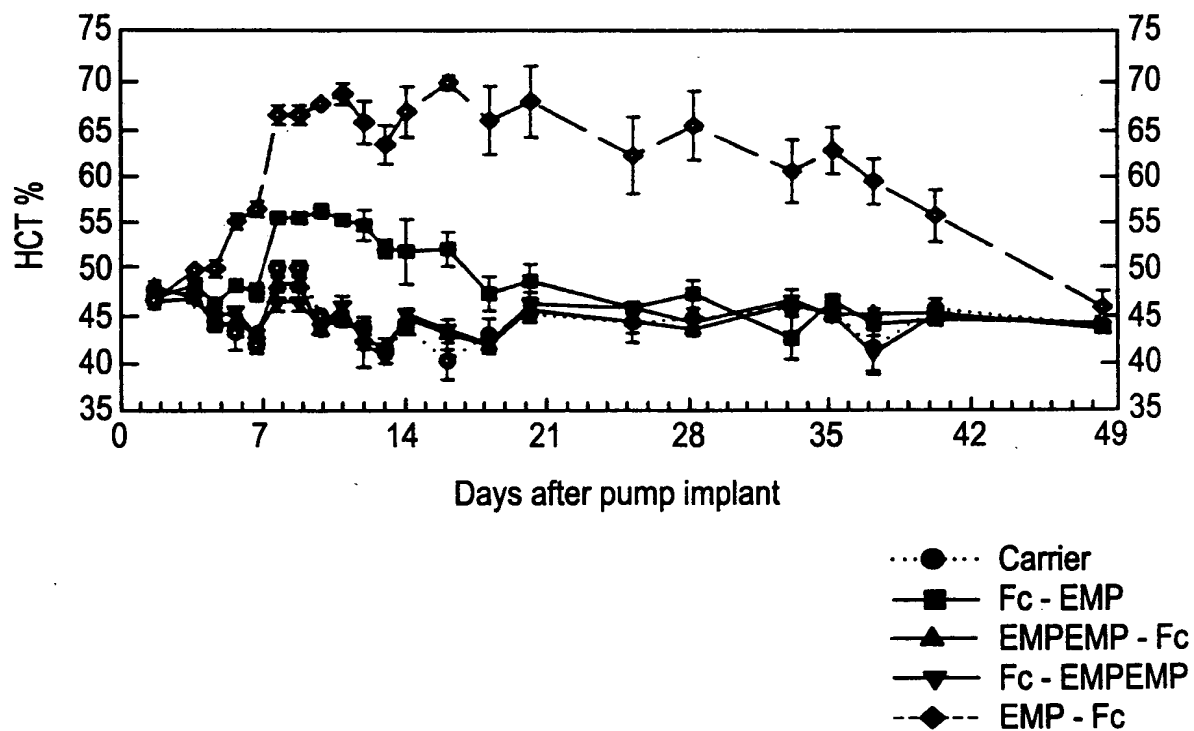


FIG. 19A

NdeI

```

1  CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCG
   -----+-----+-----+-----+-----+-----+-----+
a   M D K T H T C P P C P A P E L L G G P
61  TCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
   -----+-----+-----+-----+-----+-----+-----+
a   S V F L F P P K P K D T L M I S R T P E
121 AGTCAGAAGGAGAAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC
   -----+-----+-----+-----+-----+-----+-----+
a   V T C V V V D V S H E D P E V K F N W Y
181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
   -----+-----+-----+-----+-----+-----+-----+
a   V D G V E V H N A K T K P R E E Q Y N S
241 ACGTACCGTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
   -----+-----+-----+-----+-----+-----+-----+
a   T Y R V V S V L T V L H Q D W L N G K E
301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
   -----+-----+-----+-----+-----+-----+-----+
a   Y K C K V S N K A L P A P I E K T I S K
361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
   -----+-----+-----+-----+-----+-----+-----+
a   A K G Q P R E P Q V Y T L P P S R D E L
421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
   -----+-----+-----+-----+-----+-----+-----+
a   T K N Q V S L T C L V K G F Y P S D I A
481 TGGTTCCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
   -----+-----+-----+-----+-----+-----+-----+
a   V E W E S N G Q P E N N Y K T T P P V L
541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
   -----+-----+-----+-----+-----+-----+-----+
a   D S D G S F F L Y S K L T V D K S R W Q
600 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCAGTGGCACCTGTTCTCGTCCACCGTC

```

FIG. 19B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
-----+-----+-----+-----+-----+-----+
a   GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
    Q G N V F S C S V M H E A L H N H Y T Q -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC 720
-----+-----+-----+-----+-----+-----+
a   TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCACTGAAGGACGGCGTGATG
    K S L S L S P G K G G G G G D F L P H Y -

                                BamHI
                                |
721 AAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC 757
-----+-----+-----+-----+
a   TTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG
    K N T S L G H R P *
```

FIG. 20A

NdeI
|
1 CATATGGACTTCCTGCCGCACTACAAAAACACCTCTCTGGGTCACCGTCCGGGTGGAGGC 60
-----+-----+-----+-----+-----+-----+
GTATACCTGAAGGACGGCGTGATGTTTTTGTGGAGAGACCCAGTGGCAGGCCACCTCCG
a M D F L P H Y K N T S L G H R P G G G -
61 GGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG 120
-----+-----+-----+-----+-----+-----+
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGC
a G G D K T H T C P P C P A P E L L G G P -
121 TCAGTTTTCTCTTCCCCCAAACCCAAGGACACCTCATGATCTCCCGGACCCCTGAG 180
-----+-----+-----+-----+-----+-----+
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
181 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 240
-----+-----+-----+-----+-----+-----+
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
241 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 300
-----+-----+-----+-----+-----+-----+
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC
a V D G V E V H N A K T K P R E E Q Y N S -
301 ACGTACCGTGTGGTCAGCGTCTCACCCTGCGCACCAGGACTGGCTGAATGGCAAGGAG 360
-----+-----+-----+-----+-----+-----+
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
361 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 420
-----+-----+-----+-----+-----+-----+
ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
421 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 480
-----+-----+-----+-----+-----+-----+
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
481 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 540
-----+-----+-----+-----+-----+-----+
TGTTTCTTGGTCCAGTCGGAAGTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
541 GTGGAGTGGGAGAGCAATGGGCAGCCGAGACAACACTACAAGACCACGCCTCCCGTGCTG 600
-----+-----+-----+-----+-----+-----+
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -

FIG. 20B

```

601 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 660
-----+-----+-----+-----+-----+
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC

a   D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 720
-----+-----+-----+-----+-----+
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG 761
-----+-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC

a   K S L S L S P G K *
```


FIG. 21B

```

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGGT
-----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA

a   K   S   L   S   L   S   P   G   K   G   G   G   G   G   F   E   W   T   P   G   -

                                     BamHI
                                     |
721 TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
-----+-----+-----+-----+-----+ 763
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC

a   Y   W   Q   P   Y   A   L   P   L   *
```

FIG. 22A

NdeI
|
CATATGTTTCGAATGGACCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG

a M F E W T P G Y W Q P Y A L P L G G G -

GGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG
61 -----+-----+-----+-----+-----+-----+-----+ 120
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGC

a G G D K T H T C P P C P A P E L L G G P -

TCAGTTTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
121 -----+-----+-----+-----+-----+-----+-----+ 180
AGTCAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
181 -----+-----+-----+-----+-----+-----+-----+ 240
CAGTGACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
241 -----+-----+-----+-----+-----+-----+-----+ 300
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG

a V D G V E V H N A K T K P R E E Q Y N S -

ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
301 -----+-----+-----+-----+-----+-----+-----+ 360
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA
361 -----+-----+-----+-----+-----+-----+-----+ 420
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
421 -----+-----+-----+-----+-----+-----+-----+ 480
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

ACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
481 -----+-----+-----+-----+-----+-----+-----+ 540
TGGTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCTCCCGTGCTG
541 -----+-----+-----+-----+-----+-----+-----+ 600
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGTATGTTCTGGTGGGAGGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

FIG. 22B

```

601 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+-----+ 660
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a   D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 720
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
-----+-----+-----+-----+-----+ 757
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG

a   K S L S L S P G K *
```

FIG. 23A

NdeI
 |
 CATATGGACAAAACCTCACACATGTCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCG
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 GTATACCTGTTTGTAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

TCAGTTTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
 61 -----+-----+-----+-----+-----+-----+-----+ 120
 AGTCAAAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
 121 -----+-----+-----+-----+-----+-----+-----+ 180
 CAGTGACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
 181 -----+-----+-----+-----+-----+-----+-----+ 240
 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG

a V D G V E V H N A K T K P R E E Q Y N S -

ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
 241 -----+-----+-----+-----+-----+-----+-----+ 300
 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAA
 301 -----+-----+-----+-----+-----+-----+-----+ 360
 ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
 361 -----+-----+-----+-----+-----+-----+-----+ 420
 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
 421 -----+-----+-----+-----+-----+-----+-----+ 480
 TGGTTCCTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTG
 481 -----+-----+-----+-----+-----+-----+-----+ 540
 CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
 541 -----+-----+-----+-----+-----+-----+-----+ 600
 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 23B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
-----+-----+-----+-----+-----+-----+
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGGTGAACCGAACTGTGAC 720
-----+-----+-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACCTGGCTTGACACTG

a      K  S  L  S  L  S  P  G  K  G  G  G  G  G  V  E  P  N  C  D  -

                                           BamHI
                                           |
721 ATCCATGTTATGTGGGAATGGGAATGTTTTGAACGTCTGTAACCTCGAGGATCC 773
-----+-----+-----+-----+-----+-----+
TAGGTACAATACACCCTTACCCTTACAAAACCTGCAGACATTGAGCTCCTAGG

a      I  H  V  M  W  E  W  E  C  F  E  R  L  *
```

FIG. 24A

NdeI
|
1 CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTGAACGT 60
-----+-----+-----+-----+-----+-----+-----+
GTATACCAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACCTGCA
a M V E P N C D I H V M W E W E C F E R -
61 CTGGGTGGTGGTGGTGGTGACAAAACCTCACACATGTCCACCGTGCCAGCACCTGAACTC 120
-----+-----+-----+-----+-----+-----+-----+
GACCCACCACCACCACCACTGTTTTGAGTGTGTACAGGTGGCACGGGTTCGTGGACTTGAG
a L G G G G G D K T H T C P P C P A P E L -
121 CTGGGGGGACCGTCAGTTTTCCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCC 180
-----+-----+-----+-----+-----+-----+-----+
GACCCCCCTGGCAGTCAAAAGGAGAAGGGGGTTCCTGTGGGAGTACTAGAGG
a L G G P S V F L F P P K P K D T L M I S -
181 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAG 240
-----+-----+-----+-----+-----+-----+-----+
GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC
a R T P E V T C V V V D V S H E D P E V K -
241 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 300
-----+-----+-----+-----+-----+-----+-----+
AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC
a F N W Y V D G V E V H N A K T K P R E E -
301 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 360
-----+-----+-----+-----+-----+-----+-----+
GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC
a Q Y N S T Y R V V S V L T V L H Q D W L -
361 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAA 420
-----+-----+-----+-----+-----+-----+-----+
TTACCGTTCCTCATGTTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT
a N G K E Y K C K V S N K A L P A P I E K -
421 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 480
-----+-----+-----+-----+-----+-----+-----+
TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG
a T I S K A K G Q P R E P Q V Y T L P P S -
481 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 540
-----+-----+-----+-----+-----+-----+-----+
GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGG
a R D E L T K N Q V S L T C L V K G F Y P -
541 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACG 600
-----+-----+-----+-----+-----+-----+-----+
TCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTG
a S D I A V E W E S N G Q P E N N Y K T T -

FIG. 24B

```
601 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG 660
    .....+.....+.....+.....+.....+.....+.....+
a   P P V L D S D G S F F L Y S K L T V D K -

    AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC
661 .....+.....+.....+.....+.....+.....+.....+ 720
    TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG

a   S R W Q Q G N V F S C S V M H E A L H N -

                                     BamHI
                                     |
    CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC
721 .....+.....+.....+.....+.....+.....+ 773
    GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG

a   H Y T Q K S L S L S P G K *
```

FIG. 25A

NdeI
 |
 1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG 60
 -----+-----+-----+-----+-----+-----+-----+-----+
 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

61 TCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
 -----+-----+-----+-----+-----+-----+-----+-----+
 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
 -----+-----+-----+-----+-----+-----+-----+-----+
 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
 -----+-----+-----+-----+-----+-----+-----+-----+
 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC

a V D G V E V H N A K T K P R E E Q Y N S -

241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
 -----+-----+-----+-----+-----+-----+-----+-----+
 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA 360
 -----+-----+-----+-----+-----+-----+-----+-----+
 ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
 -----+-----+-----+-----+-----+-----+-----+-----+
 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
 -----+-----+-----+-----+-----+-----+-----+-----+
 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATAAGACCACGCCTCCCGTGCTG 540
 -----+-----+-----+-----+-----+-----+-----+-----+
 CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
 -----+-----+-----+-----+-----+-----+-----+-----+
 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 25B

```

CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
601 -----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -
      AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCACTGGGGT
661 -----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA
A      K  S  L  S  L  S  P  G  K  G  G  G  G  G  C  T  T  H  W  G  -
      BamHI
      |
      TTCACCCTGTGCTAATGGATCCCTCGAG
721 -----+-----+-----+-----+-----+ 748
      AAGTGGGACACGATTACCTAGGGAGCTC
a      F  T  L  C  *
```

FIG. 26A

NdeI
|
1 CATATGTGCACCACCCACTGGGGTTTCACCCTGTGCGGTGGAGGCGGTGGGGACAAAGGT 60
GTATACACGTGGTGGGTGACCCCAAAGTGGGACACGCCACCTCCGCCACCCCTGTTTCCA
a M C T T H W G F T L C G G G G G D K G -
61 GGAGGCGGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGG 120
CCTCCGCCACCCCTGTTTGTAGTGTGTACAGGTGGAACGGGTGCTGGACTTGAGGACCC
a G G G G D K T H T C P P C P A P E L L G -
121 GGACCGTCAGTTTTCTCTTCCCCCAAACCCAAAGGACACCCTCATGATCTCCCGGACC 180
CCTGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGG
a G P S V F L F P P K P K D T L M I S R T -
181 CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC 240
GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG
a P E V T C V V V D V S H E D P E V K F N -
241 TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC 300
ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG
a W Y V D G V E V H N A K T K P R E E Q Y -
301 AACAGCACGTACCGTGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAATGGC 360
TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG
a N S T Y R V V S V L T V L H Q D W L N G -
361 AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATC 420
TTCCTCATGTTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG
a K E Y K C K V S N K A L P A P I E K T I -
421 TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT 480
AGGTTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTA
a S K A K G Q P R E P Q V Y T L P P S R D -
481 GAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC 540
CTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTG
a E L T K N Q V S L T C L V K G F Y P S D -
541 ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCC 600
TAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGG
a I A V E W E S N G Q P E N N Y K T T P P -

FIG. 26B

```

601 GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCCTGGACAAGAGCAGG
-----+-----+-----+-----+-----+-----+ 660
CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCC
a   V L D S D G S F F L Y S K L T V D K S R -

TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
661 -----+-----+-----+-----+-----+ 720
ACCGTCGTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG
a   W Q Q G N V F S C S V M H E A L H N H Y -

                                     BamHI
                                     |
ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721 -----+-----+-----+-----+-----+ 763
TGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a   T Q K S L S L S P G K *
```